STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

Source:

Date Processed by STIC:

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u> <u>VERSION 4.4.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>, EFS Submission User Manual ePAVE)
- 2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
- Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
 U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street,
 Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER: 0785,621
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE	
lWrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters , instead.
4Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5Variable Length	Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7Skipped Sequences . (OLD RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
8Skipped Sequences (NEW RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000
9Use of n's or Xaa's OEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
10 V Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
11Use of <220>	Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of Patentln version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13 Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFW16

RAW SEQUENCE LISTING DATE: 05/15/2006
PATENT APPLICATION: US/10/785,621 TIME: 15:51:40

Input Set : A:\10991588-2.txt

Output Set: N:\CRF4\05152006\J785621.raw

```
3 <110> APPLICANT: Agilent Technologies
         Myerson, Joel
 6 <120> TITLE OF INVENTION: Increasing Ionization Efficiency in Mass Spectrometry
 8 <130> FILE REFERENCE: 10991588-2
                                            TryAlid Does Not Comply
Corrected Diskette Needed;
Response (Pg.1-2)
ron summary sueet.
10 <140> CURRENT APPLICATION NUMBER: 10/785,621
11 <141> CURRENT FILING DATE: 2004-02-23
13 <160> NUMBER OF SEQ ID NOS: 6
15 <170> SOFTWARE: PatentIn version 3.3
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 4
19 <212> TYPE: PRT
20 <213> ORGANISM: (Chemically Synthesized
22 <400> SEQUENCE: 1
24 Lys Ala Lys Ala
25 1
28 <210> SEQ ID NO: 2
29 <211> LENGTH: 9
30 <212> TYPE: PRT
31 <213> ORGANISM: (Chemically Synthesized)
33 <400> SEQUENCE: 2
                                                                         12137
Responses
CAN Only
be either
35 Lys Gly Gly Gly Lys Gly Gly Lys
39 <210> SEQ ID NO: 3
40 <211> LENGTH: 9
41 <212> TYPE: PRT
42 <213> ORGANISM Chemically Synthesized
44 <400> SEQUENCE:
46 Lys Ala Lys Ala Lys Leu Lys Val Lys 🔇
47 1
50 <210> SEQ ID NO: 4
51 <211> LENGTH: 6
52 <212> TYPE: PRT
53 <213> ORGANISM Chemically Synthesized
56 <220> FEATURE:
57 <221> NAME/KEY: Variant
58 <222> LOCATION: (1)..(1)
59 <223> OTHER INFORMATION: X=N-Trimethyl Lysine
61 <220> FEATURE:
62 <221> NAME/KEY: Variant
63 <222> LOCATION: (3)..(3)
64 <223> OTHER INFORMATION: X=N-Trimethyl Lysine
66 <220> FEATURE:
67 <221> NAME/KEY: Variant
```

Seeiten #10 on error Summary Sheet

```
RAW SEQUENCE LISTING
                                                               DATE: 05/15/2006
                     PATENT APPLICATION: US/10/785,621
                                                               TIME: 15:51:40
                      Input Set : A:\10991588-2.txt
                     Output Set: N:\CRF4\05152006\J785621.raw
     68 <222> LOCATION: (5)..(5)
     69 <223> OTHER INFORMATION: X=N-Trimethyl Lysine
     71 <400> SEQUENCE: 4
W--> 73 Xaa Gly Xaa Gly Xaa Gly
                                                    Invalid
Response
     74 1
     77 <210> SEQ ID NO: 5
     78 <211> LENGTH: 7
     79 <212> TYPE: PRT
     80 <213> ORGANISM: (Chemically Synthesized
     83 <220> FEATURE:
     84 <221> NAME/KEY: Variant
     85 <222> LOCATION: (1)..(1)
     86 <223> OTHER INFORMATION: X=N-Trimethyl Lysine
                                                                               See item
#10 00
error
summary
Sheeti
     88 <220> FEATURE:
     89 <221> NAME/KEY: Variant
     90 <222> LOCATION: (4)..(4)
     91 <223> OTHER INFORMATION: X=N-Trimethyl Lysine
     93 <220> FEATURE:
     94 <221> NAME/KEY: Variant
     95 <222> LOCATION: (7)..(7)
     96 <223> OTHER INFORMATION: X=N-Trimethyl Lysine
     98 <400> SEQUENCE: 5
W--> 100 Xaa Ala Ala Xaa Ala Ala Xaa
     101 1
     104 <210> SEQ ID NO: 6
     105 <211> LENGTH: 7
     106 <212> TYPE: PRT
     107 <213> ORGANISM: (Chemically Synthesized
     110 <220> FEATURE:
     111 <221> NAME/KEY: Variant
     112 <222> LOCATION: (1)..(1)
     113 <223> OTHER INFORMATION: X=N-Trimethyl Lysine
     115 <220> FEATURE:
     116 <221> NAME/KEY: Variant
     117 <222> LOCATION: (3)..(3)
     118 <223> OTHER INFORMATION: X=N-Trimethyl Lysine
     120 <220> FEATURE:
     121 <221> NAME/KEY: Variant
     122 <222> LOCATION: (5)..(5)
     123 <223> OTHER INFORMATION: X=N-Trimethyl Lysine
     125 <220> FEATURE:
     126 <221> NAME/KEY: Variant
     127 <222> LOCATION: (7)..(7)
     128 <223> OTHER INFORMATION: X=N-Trimethyl Lysine
     130 <400> SEQUENCE: 6
W--> 132 Xaa Leu Xaa Val Xaa Gly Xaa
     133 1
                                                                The type of errors shown exist throughout
```

the Sequence Listing. Please check subsequent

sequences for similar errors.

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/785,621

DATE: 05/15/2006 TIME: 15:51:41

Input Set : A:\10991588-2.txt

Output Set: N:\CRF4\05152006\J785621.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:4; Xaa Pos. 1,3,5 Seq#:5; Xaa Pos. 1,4,7

Seq#:6; Xaa Pos. 1,3,5,7 \(\infty \)

VERIFICATION SUMMARY

DATE: 05/15/2006

PATENT APPLICATION: US/10/785,621

TIME: 15:51:41

Input Set : A:\10991588-2.txt

Output Set: N:\CRF4\05152006\J785621.raw

L:73 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0 L:100 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0 L:132 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0